

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/069,772 A
Source: IFWO
Date Processed by STIC: 2/24/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

10/06 9,772 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 **Wrapped Nucleics** The number/letter at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 **Misaligned Amino** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 **PatentIn 2.0** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 **Skipped Sequences** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (OLD RULES)
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 **Skipped Sequences** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. (NEW RULES)
<210> sequence id number
<400> sequence id number
000

9 **Use of n's or Xaa's** Use of n's and/or Xaa's have been detected in the Sequence Listing. (NEW RULES)
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 **Invalid <213>** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11 **Use of <220>** Sequence(s) 1 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12 **PatentIn 2.0** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

2/24/20

RAW SEQUENCE LISTING

DATE: 02/24/2006

PATENT APPLICATION: US/10/069,772A

TIME: 15:43:05

Input Set : F:\Feussner-10069772-060211-SEQLIST.txt

Output Set : N:\CRF4\02242006\J069772A.raw

```

58 Cys Gly His His Ala Phe Ser Asp Tyr Gln Leu Ile Asp Asp Ile Val
59          105          110          115
61 gga ttc gtg ctc cat tcg gct ctc acc ccg tat ttc tct tgg aaa 440
62 Gly Phe Val Leu His Ser Ala Leu Thr Pro Tyr Phe Ser Trp Lys
63          120          125          130
65 tat agc cac agg aat cac cac gcc aac aca aat tca ctc gat aac gat 488
67 Tyr Ser His Arg Asn His His Ala Asn Thr Asn Ser Leu Asp Asn Asp
68          135          140          145
70 gaa gtt tac att cct aaa cgt aag tcg aag gtc aag att tat tcc aaa 536
71 Glu Val Tyr Ile Pro Lys Arg Lys Ser Lys Val Lys Ile Tyr Ser Lys
72 150          155          160          165
74 ctt ctt aac aat cca ccc ggg cga gtg ttc act ttg gtg ttt cgg ttg 584
75 Leu Leu Asn Asn Pro Pro Gly Arg Val Phe Thr Leu Val Phe Arg Leu
76          170          175          180
78 act tta gga ttt ccg tta tac ctc tta act aat atc tcg ggc aag aaa 632
79 Thr Leu Gly Phe Pro Leu Tyr Leu Thr Asn Ile Ser Gly Lys Lys
80          185          190          195
82 tac ggg agg ttt gcc aac cac ttt gat ccc atg agt cca att ttc aac 680
83 Tyr Gly Arg Phe Ala Asn His Phe Asp Pro Met Ser Pro Ile Phe Asn
84          200          205          210
86 gat cgt gaa cgc gtt caa gtt ttg cta tcc gat ttc ggt ctt ctc gct 728
87 Asp Arg Glu Arg Val Gln Val Leu Leu Ser Asp Phe Gly Leu Leu Ala
88          215          220          225
90 gta ttt tat gca atc aag ctt ctt gta gca gca aaa ggg gca gct tgg 776
91 Val Phe Tyr Ala Ile Lys Leu Leu Val Ala Ala Lys Gly Ala Ala Trp
92 230          235          240          245
94 gta atc aac atg tac gca att cca gta cta ggt gta agc gtg ttc ttc 824
95 Val Ile Asn Met Tyr Ala Ile Pro Val Leu Gly Val Ser Val Phe Phe
96          250          255          260
99 gtt ttg atc aca tat ttg cac cac acc cat ctc tca ctc cct cat tat 872
100 Val Leu Ile Thr Tyr Leu His His Thr His Leu Ser Leu Pro His Tyr
101          265          270          275
103 gat tca acc gaa tgg aac tgg atc aaa ggc gcc tta tca aca atc gat 920
104 Asp Ser Thr Glu Trp Asn Trp Ile Lys Gly Ala Leu Ser Thr Ile Asp
105          280          285          290
107 agg gat ttc ggg ttc ctg aat cgg gtt ttc cac gac gtt aca cac act 968
108 Arg Asp Phe Gly Phe Leu Asn Arg Val Phe His Asp Val Thr His Thr
109          295          300          305
111 cac gtc ttg cat cat ttg atc tca tac att cca cat tat cat gca aag 1016
112 His Val Leu His His Leu Ile Ser Tyr Ile Pro His Tyr His Ala Lys
113 310          315          320          325
115 gaa gca agg gat gca atc aag cca gtg ttg ggc gag tac tat aaa atc 1064
116 Glu Ala Arg Asp Ala Ile Lys Pro Val Leu Gly Glu Tyr Tyr Lys Ile
117          330          335          340
119 gac agg act cca att ttc aaa gca atg tat aga gag gct aag gaa tgc 1112
120 Asp Arg Thr Pro Ile Phe Lys Ala Met Tyr Arg Glu Ala Lys Glu Cys
121          345          350          355
123 atc tac atc gag ccc gat gag gat agc gag cac aaa ggt gtg ttc tgg 1160
124 Ile Tyr Ile Glu Pro Asp Glu Asp Ser Glu His Lys Gly Val Phe Trp

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125          360          365          370
127 tac cac aag atg taa tcaaaaagggt gtagtgcaat gcaattgtat gcttaattaa 1215
128 Tyr His Lys Met
130          375
132 gttggttaaac tttctattcc gtgtaataaa ttatcattaa gagaaaaaaa aaaaaaaaaa 1275
134 aaaaaaaaaa 1285
137 <210> SEQ ID NO: 2
138 <211> LENGTH: 377
139 <212> TYPE: PRT
140 <213> ORGANISM: Calendula officinalis
143 <400> SEQUENCE: 2
144 Met Gly Ala Gly Gly Arg Met Ser Asp Pro Ser Glu Gly Lys Asn Ile
145 1 5 10 15
147 Leu Glu Arg Val Pro Val Asp Pro Pro Phe Thr Leu Ser Asp Leu Lys
148 20 25 30
150 Lys Ala Ile Pro Thr His Cys Phe Glu Arg Ser Val Ile Arg Ser Ser
151 35 40 45
153 Tyr Tyr Val Val His Asp Leu Ile Val Ala Tyr Val Phe Tyr Tyr Leu
154 50 55 60
156 Ala Asn Thr Tyr Ile Pro Leu Ile Pro Thr Pro Leu Ala Tyr Leu Ala
157 65 70 75 80
159 Trp Pro Val Tyr Trp Phe Cys Gln Ala Ser Ile Leu Thr Gly Leu Trp
160 85 90 95
163 Val Ile Gly His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Leu
164 100 105 110
166 Ile Asp Asp Ile Val Gly Phe Val Leu His Ser Ala Leu Leu Thr Pro
167 115 120 125
169 Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn
170 130 135 140
172 Ser Leu Asp Asn Asp Glu Val Tyr Ile Pro Lys Arg Lys Ser Lys Val
173 145 150 155 160
175 Lys Ile Tyr Ser Lys Leu Leu Asn Asn Pro Pro Gly Arg Val Phe Thr
176 165 170 175
178 Leu Val Phe Arg Leu Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn
179 180 185 190
181 Ile Ser Gly Lys Lys Tyr Gly Arg Phe Ala Asn His Phe Asp Pro Met
182 195 200 205
184 Ser Pro Ile Phe Asn Asp Arg Glu Arg Val Gln Val Leu Leu Ser Asp
185 210 215 220
187 Phe Gly Leu Leu Ala Val Phe Tyr Ala Ile Lys Leu Leu Val Ala Ala
188 225 230 235 240
190 Lys Gly Ala Ala Trp Val Ile Asn Met Tyr Ala Ile Pro Val Leu Gly
191 245 250 255
194 Val Ser Val Phe Phe Val Leu Ile Thr Tyr Leu His His Thr His Leu
195 260 265 270
197 Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Lys Gly Ala
198 275 280 285
200 Leu Ser Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg Val Phe His
201 290 295 300

```

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Input Set : F:\Feussner-10069772-060211-SEQLIST.txt

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203 Asp Val Thr His Thr His Val Leu His His Leu Ile Ser Tyr Ile Pro
204 305 310 315 320
206 His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Val Leu Gly
207 325 330 335
209 Glu Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Phe Lys Ala Met Tyr Arg
210 340 345 350
212 Glu Ala Lys Glu Cys Ile Tyr Ile Glu Pro Asp Glu Asp Ser Glu His
213 355 360 365
215 Lys Gly Val Phe Trp Tyr His Lys Met
216 370 375

SEQUENCE LISTING

-> 219
-> 221 <110> APPLICANT: Feussner, Ivo
-> 221 <110> APPLICANT: Feussner, Ivo
-> 226 <120> TITLE OF INVENTION: Fatty acid desaturase gene from plants
-> 226 <120> TITLE OF INVENTION: Fatty acid desaturase gene from plants
-> 228 <130> FILE REFERENCE: 50669
-> 228 <130> FILE REFERENCE: 50669
-> 230 <140> CURRENT APPLICATION NUMBER: US 10/069,772A
-> 231 <141> CURRENT FILING DATE: 2002-02-28
-> 233 <160> NUMBER OF SEQ ID NOS: 14
-> 233 <160> NUMBER OF SEQ ID NOS: 14
-> 235 <170> SOFTWARE: PatentIn version 3.3

See error
Explanation
on page 5.

↓ This is from sequence 2

Lys Gly Val Phe Trp Tyr His Lys Met
370 375

SEQUENCE LISTING

<110> Feussner, Ivo
Hornung, Ellen
Fritzsche, Kathrin
Peitzsch, Nicola

<120> Fatty acid desaturase gene from plants

<130> 50669

<140> US 10/069,772

<141> 2002-02-28

<160> 14

<170> PatentIn version 3.3

<210> 3

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 3

ccdrtyttct ctggaarwhh agycaycg

- This Appeared after
Sequence 2.

- Per Sequence rules,
Show <110> - <170>
only at the beginning
of the sequence listing.

- Delete <110> - <170> from
this section.

<210> 6
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (13)..(13)
 <223> n is inositol

<400> 6
 ccartyccay tcnqwbgart crtartg

"N" CAN represent only a nucleotide, Not
 an alcohol.

27

Invalid
 response

p/s see item # 13 on error summary
 Sheet.

<210> 15

<211> 28

<212> DNA

<213> Artificial Sequence

pls explain source of genetic material.

<220>

<223> none

Invalid Response

<400> 15

tattccaaac ttcttaacaa tccacccg

See item # 11

<210> 16

<211> 28

<212> DNA

<213> Artificial Sequence

on error summary sheet,

<220>

<223> none

Same error

<400> 16

caattccagt actaggtgta agtgtgtt

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/069,772A

DATE: 02/24/2006
TIME: 15:43:06

Input Set : F:\Feussner-10069772-060211-SEQLIST.txt
Output Set: N:\CRF4\02242006\J069772A.raw

valid Line Length:

rules require that a line not exceed 72 characters in length. This includes spaces.

1# : 1; Line(s) 24,28,29,30,31,32,33,34,36,37,38,39,40,41,42,43,44,45,46,47
1# : 1; Line(s) 48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,67,68
1# : 1; Line(s) 69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88
1# : 1; Line(s) 89,90,91,92,93,94,95,96,97,99,100,101,102,103,104,105,106
1# : 1; Line(s) 107,108,109,110,111,112,113,114,115,116,117,118,119,120,121
1# : 1; Line(s) 122,123,124,125,126,127,128,130,131,132,133
1# : 2; Line(s) 138,139,144,145,146,147,148,149,150,151,152,153,154,155,156
1# : 2; Line(s) 157,158,159,160,161,163,164,165,166,167,168,169,170,171,172
1# : 2; Line(s) 173,174,175,176,177,178,179,180,181,182,183,184,185,186,187
1# : 2; Line(s) 188,189,190,191,192,194,195,196,197,198,199,200,201,202,203
1# : 2; Line(s) 204,205,206,207,208,209,210,211,212,213,214,215

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VERIFICATION SUMMARY

DATE: 02/24/2006

PATENT APPLICATION: US/10/069,772A

TIME: 15:43:06

Input Set : F:\Feussner-10069772-060211-SEQLIST.txt

Output Set: N:\CRF4\02242006\J069772A.raw

27 M:282 E: Numeric Field Identifier Missing, <213> is required. /
27 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:1 /
219 M:333 E: Wrong sequence grouping, Amino acids not in groups! /
219 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:2 //
219 M:252 E: No. of Seq. differs, <211> LENGTH:Input:377 Found:379 SEQ:2 /
221 M:280 W: Numeric Identifier already exists, <110> found multiple times /
221 M:281 W: Numeric Fields not Ordered, <110> not ordered!. /
226 M:280 W: Numeric Identifier already exists, <120> found multiple times /
226 M:281 W: Numeric Fields not Ordered, <120> not ordered!. /
228 M:280 W: Numeric Identifier already exists, <130> found multiple times /
228 M:281 W: Numeric Fields not Ordered, <130> not ordered!. /
230 M:280 W: Numeric Identifier already exists, <140> found multiple times /
230 M:281 W: Numeric Fields not Ordered, <140> not ordered!. /
231 M:280 W: Numeric Identifier already exists, <141> found multiple times /
231 M:281 W: Numeric Fields not Ordered, <141> not ordered!. /
233 M:280 W: Numeric Identifier already exists, <160> found multiple times /
233 M:281 W: Numeric Fields not Ordered, <160> not ordered!. /
235 M:280 W: Numeric Identifier already exists, <170> found multiple times /
288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0 /
233 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (14) Counted (16) /